CURRICULUM VITAE

Date of Revision: August 31, 2017

Name James P. Noonan, Ph.D.

Education

B.S.	Biology and English Literature, State University of New York at Binghamton, 1997
Ph.D.	Genetics, Stanford University School of Medicine, 2004 Thesis: *The evolution of protocadherin gene cluster diversity* Advisor: Richard M. Myers, Ph.D.

Career/Academic Appointments

2004-2007	Postdoctoral Fellow, Genomics Division, Lawrence Berkeley National Laboratory, Berkeley, CA Advisor: Edward M. Rubin, M.D., Ph.D.
2007-2013	Assistant Professor, Department of Genetics, Yale School of Medicine, New Haven, CT
2013-2014	Associate Professor, Department of Genetics, Yale School of Medicine, New Haven, CT
2014-2016	Associate Professor, Department of Genetics and Department of Ecology and Evolutionary Biology, Yale University
2016-present	Associate Professor (tenure), Department of Genetics and Department of Ecology and Evolutionary Biology, Yale University
2016-present	Executive Director for Genome Sciences, Yale Center for Genome Analysis

Professional Honors and Recognition

International/National/Regional

2008	Career Award, Edward Mallinckrodt Jr. Foundation
2004	NIH NRSA Postdoctoral Fellowship
1997	Phi Beta Kappa, State University of New York at Binghamton

Grant History

Active

Agency:	NIH-NIGMS
ID#:	R01 GM094780-08
Title:	"Identifying enhancers with human-specific developmental functions"
P.I.	James P. Noonan
Direct costs per year:	$390,830
Percent effort:	50%
Total costs for project period:	$6,364,543

Project period: 08/01/2010 - 07/31/2019

Agency: Simons Foundation
ID#: 512694
Title: "Mapping ASD regulatory networks at cellular resolution in neurodevelopment"
P.I. James P. Noonan
Direct costs per year: $220,000
Percent effort: 10%
Total costs for project period: $825,000
Project period: 09/01/17-/08/31/20

Agency: Charles Hood Foundation
Title: "Discovering gene regulatory networks in early human brain development that contribute to autism spectrum disorder"
P.I. James P. Noonan
Direct costs per year: $204,545
Percent effort: 10%
Total costs for project period: $450,000
Project period: 01/01/16-12/31/17

Agency: NIH-NIDA
ID# R01 DA023999-07
Title: "Origin of cortical species-specific distinctions"
P.I. Pasko Rakic
Role on project: Co-Investigator
Direct costs per year: $17,857
Percent effort: 9%
Total costs for project period: $7,562,902
Project period: 12/1/2007 - 02/28/2019

Agency: NIH-NEI
ID# R01 EY002593-30
Title: "Prenatal development of the visual system"
P.I. Pasko Rakic
Role on project: Co-Investigator
Direct costs per year: $9,708
Percent effort: 5%
Total costs for project period: $2,858,938
Project period: 9/30/2014-8/31/2018

Past

Agency: Simons Foundation
ID#: 274624
Title: "A gene-driven systems biological approach to ASD pathology"
P.I. Matthew State, Nenad Sestan, James P. Noonan, Kathryn Roeder
Total costs for project period: $1,258,251
Project period: 08/01/2013-07/31/2016

Agency: NIH-NIMH
ID#: RC2 MH089929
Title: "Transcriptional atlas of human brain development"
P.I. Nenad Sestan
Role on project: Co-Investigator
Total costs for project period: $9,889,558
Project period: 09/30/2009 - 08/31/2012

Agency: Edward Mallinckrodt, Jr. Foundation
ID# Career Award
Title: "Elucidating the regulatory architecture of development using enhancer target capture"
P.I. James P. Noonan
Total costs for project period: $180,000
Project period: 10/1/2008 - 09/30/2011

Invited Speaking Engagements, Presentations, Symposia and Workshops not Affiliated with Yale

International/National

2017	Simons Foundation Autism Research Initiative Annual Meeting, New York, NY "Discovering *CHD8* regulatory networks disrupted in autism"
2017	ASBMB Special Symposium: Evolution and Core Processes in Gene Expression Stowers Institute "Genetic models of human evolution"
2017	Society for Molecular Biology and Evolution Annual Conference, Invited Symposium "Genetic models of human evolution"
2017	"Science at the Edge" Seminar Series, Michigan State University "Genetic models of human evolution"
2017	BBC Graduate Programs Seminar Series, University of California, San Francisco "Genetic models of human evolution"
2015	CSHL Meeting: Behavior and Neurogenetics of Nonhuman Primates "Comparative epigenetic analysis of early primate cortical development"
2015	Stanley Center for Cognitive Genomics, Cold Spring Harbor Laboratory "Gene regulatory mechanisms in human cognition and its disorders"
2015	Department of Biology and the Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD "Evolution of distinctly human phenotypes"
2014	Molecular Psychiatry 2nd Annual Conference, San Francisco, CA "Regulatory convergence in Autism Spectrum Disorder"
2014	The Jackson Laboratory for Genomic Medicine, Farmington, CT "Long-range regulatory interactions during embryonic development"
2014	Simons Foundation Autism Research Initiative Annual Meeting, New York, NY "Regulatory convergence in Autism Spectrum Disorder"

2014	Society for Molecular Biology and Evolution Annual Conference, Invited Symposium, "Evolution of the human developmental regulome"
2014	Advances in Genome Biology and Technology Annual Meeting, Marco Island, FL "Epigenomic analysis in the developing human embryo"
2013	Department of Genetics, University of Pennsylvania, Philadelphia, PA "Evolution of the human developmental regulome"
2013	Society for Molecular Biology and Evolution Annual Conference, Invited Symposium, "The molecular basis of human traits"
2013	Department of Genome Sciences, University of Washington, Seattle, WA "Human-specific gene regulation in the developing embryo"
2013	Department of Anthropology, University of New Mexico, Albuquerque, NM "The evolution of human-specific developmental gene regulation"
2012	Department of Developmental Biology, Stanford University, Palo Alto, CA "Evolution of the human developmental regulome"
2012	Department of Human Genetics, University of Chicago, Chicago, IL "Deciphering uniquely human developmental gene regulation"
2011	Genome Institute of Singapore, Singapore "Deciphering uniquely human gene regulation"
2011	22nd Meeting of the German Society of Human Genetics, Regensburg, Germany "Gene regulation and the origins of human biological uniqueness"
2011	CARTA Symposium: The Genetics of Humanness, San Diego, CA "Uniquely human gene regulation"
2011	Advances in Genome Biology and Technology Meeting, Marco Island, FL "Next generation sequencing at the Yale Center for Genome Analysis"
2011	Genome Sciences Symposia, Lawrence Berkeley National Laboratory "Deciphering uniquely human gene regulation"
2010	McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD "Functional genomic analysis of human evolution"
2010	11th International Conference on Limb Development and Regeneration, Williamsburg, VA "Using next-generation sequencing to study gene regulation in human embryonic limb development"
2009	Human Genetics Gordon Conference, Biddeford, ME "Genome-wide identification and characterization of human-specific developmental regulatory functions"
2009	ISMB/ECCB Meeting, Stockholm, Sweden "The role of developmental *cis*-regulatory change in human evolution"
2009	National Center for Biotechnology Information, Bethesda, MD "Genome regulation and the evolution of human development"
2009	HudsonAlpha Institute for Biotechnology, Huntsville, AL "Exploring the genetic basis of human uniqueness"
2009	Department of Biology, Brandeis University, Waltham, MA "Genome regulation and the evolution of human development"

2008	CSHL Meeting: The Biology of Genomes (Session co-Chair) "Human-specific gain of function in a developmental enhancer"
2008	Department of Biology, Columbia University, New York, NY "The role of developmental gene regulatory change in human evolution"
2008	EvoS Seminar Series, State University of New York at Binghamton "Functional insights into human evolution from comparative genomics"
2008	Keystone Symposia: Complex Traits, Santa Fe, NM "Functional insights into the role of gene regulatory change in human evolution"

Peer-Reviewed Presentations & Symposia Given at Meetings Not Affiliated With Yale

International/National

2015	International Meeting for Autism Research, Salt Lake City, UT "Deciphering regulatory networks that contribute to autism risk"
2015	CSHL Meeting on Systems Biology: Global Regulation of Gene Expression "Evolutionary changes in promoter and enhancer activity during human corticogenesis"
2014	International Meeting for Autism Research "The CHD8 network in the developing brain is enriched for ASD risk genes"
2012	CSHL Meeting on Systems Biology: Global Regulation of Gene Expression: "Chromatin profiling of human embryonic tissues identifies enhancers with human-specific functions"

Professional Service

Peer Review Groups/Grant Study Sections

2015	Genome Variation and Evolution Study Section (*ad hoc*), NIH
2013	External reviewer for Wellcome Trust Investigator Award program (UK)
2013	External reviewer for NSF CAREER program
2010	Genome Canada: Large-Scale Applied Research Project Competition

Journal Service

2008-present	Reviewer for: *Science*, *Nature*, *PNAS*, *Nature Neuroscience, PLoS Genetics, Nature Reviews Genetics, Genome Research, Genome Biology*, *Molecular Biology and Evolution*, others
2008-2014	Member, Editorial Board, *Genome Research*

Service for Professional Organizations

American Society of Human Genetics

2012	Organizer, Invited Session, "Gene Regulatory Change: The Engine of Human Evolution," ASHG 62nd Annual Meeting
2010	Organizer, Invited Session, "Gene Regulation in Human Disease and Evolution," ASHG 60th Annual Meeting

Society for Molecular Biology and Evolution

2016 Organizer, Invited Symposium, "Genetic Mechanisms Influencing Morphological Evolution," SMBE Annual Meeting

Yale University Service

Yale University Committees

2012 Faculty Advisory Committee, Deputy Chief Information Officer for Academic IT candidate search

2009-2010, 2013 Admissions Committee, MCGD track, BBS

2008-present Yale Center for Genome Analysis Advisory Committee

Medical School Committees

2015 Basic Science Strategic Planning Subcommittee on Bioinformatics (YSM)

2015 Yale Center for Genome Editing Advisory Committee

2012 Faculty Advisory Committee, Deputy Chief Information Officer for Academic IT candidate search

2008-present Yale Center for Genome Analysis Advisory Committee

Departmental Committees

2014-present Genetics Faculty Search Committee

2012-present Human Genetics and Genomics Training Grant Executive Committee

Public Service

2012 Consultant, NOVA/WGBH Production, *Cracking Your Genetic Code*

2010 Featured Expert and Consultant, NOVA/WGBH Production, *What Darwin Never Knew*

Bibliography

Peer-Reviewed Original Research

1: Neff NF, Ellis NA, Ye TZ, **Noonan J**, Huang K, Sanz M, Proytcheva M. The DNA helicase activity of BLM is necessary for the correction of the genomic instability of bloom syndrome cells. *Mol. Biol. Cell* 10(3):665-76 (1999).

2: Wu Q, Zhang T, Cheng JF, Kim Y, Grimwood J, Schmutz J, Dickson M, **Noonan JP**, Zhang MQ, Myers RM, Maniatis T. Comparative DNA sequence analysis of mouse and human protocadherin gene clusters. *Genome Res*. 11(3):389-404 (2001).

3: Yankiwski V, **Noonan JP**, Neff NF. The C-terminal domain of the Bloom syndrome DNA helicase is essential for genomic stability. *BMC Cell Biol*. 2:11 (2001).

4: **Noonan JP**, Li J, Nguyen L, Caoile C, Dickson M, Grimwood J, Schmutz J, Feldman MW, Myers RM. Extensive linkage disequilibrium, a common 16.7-kilobase deletion, and evidence of balancing selection in the human protocadherin alpha cluster. *Am. J. Hum. Genet.* 72(3):621-35 (2003).

5: **Noonan JP**, Grimwood J, Schmutz J, Dickson M, Myers RM. Gene conversion and the evolution of protocadherin gene cluster diversity. *Genome Res.* 14(3):354-66 (2004).

6: Schmutz J, [47 additional authors], **Noonan JP**, Pitluck S, Pollard M, Predki P, Priest J, Ramirez L, Retterer J, Rodriguez A, Rogers S, Salamov A, Salazar A, Thayer N, Tice H, Tsai M, Ustaszewska A, Vo N, Wheeler J, Wu K, Yang J, Dickson M, Cheng JF, Eichler EE, Olsen A, Pennacchio LA, Rokhsar DS, Richardson P, Lucas SM, Myers RM, Rubin EM. The DNA sequence and comparative analysis of human chromosome 5. *Nature* 431(7006):268-74 (2004).

7: **Noonan JP**, Grimwood J, Danke J, Schmutz J, Dickson M, Amemiya CT, Myers RM. Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. *Genome Res.* 14(12):2397-405 (2004).

8: **Noonan JP**, Hofreiter M, Smith D, Priest JR, Rohland N, Rabeder G, Krause J, Detter JC, Pääbo S, Rubin EM. Genomic sequencing of Pleistocene cave bears. *Science* 309(5734):597-9 (2005).

9: Prabhakar S, **Noonan JP**, Pääbo S, Rubin EM. Accelerated evolution of conserved noncoding sequences in humans. *Science* 314(5800):786 (2006).

10: **Noonan JP**, Coop G, Kudaravalli S, Smith D, Krause J, Alessi J, Chen F, Platt D, Pääbo S, Pritchard JK, Rubin EM. Sequencing and analysis of Neanderthal genomic DNA. *Science* 314(5802):1113-8 (2006).

11: Prabhakar S, Visel A, Akiyama JA, Shoukry M, Lewis KD, Holt A, Plajzer-Frick I, Morrison H, Fitzpatrick DR, Afzal V, Pennacchio LA, Rubin EM, **Noonan JP**. Human-specific gain of function in a developmental enhancer. *Science* 321(5894):1346-50 (2008).

12. Marlatt SA, Kong Y, Cammett TJ, Korbel G, **Noonan JP**, Dimaio D. Construction and maintenance of randomized retroviral expression libraries for transmembrane protein engineering. *Protein Eng. Des. Sel.* 24(3):311-20 (2011).

13: Ayoub AE, Oh S, Xie Y, Leng J, Cotney J, Dominguez MH, **Noonan JP**, Rakic P. Transcriptional programs in transient embryonic zones of the cerebral cortex defined by high-resolution mRNA sequencing. *Proc. Natl. Acad. Sci. USA.* 108(36):14950-5 (2011).

14: Cotney J, Leng J, Oh S, DeMare LE, Reilly SK, Gerstein MB, **Noonan JP**. Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. *Genome Res.* 22(6):1069-80 (2012).

15: Bandyopadhyay U, Cotney J, Nagy M, Oh S, Leng J, Mahajan M, Mane S, Fenton WA, **Noonan JP**, Horwich AL. RNA-Seq profiling of spinal cord motor neurons from a presymptomatic SOD1 ALS mouse. *PLoS One* 8(1):e53575 (2013).

16: Clark VE, Erson-Omay EZ, Serin A, Yin J, Cotney J, Ozduman K, Avşar T, Li J, Murray PB, Henegariu O, Yilmaz S, Günel JM, Carrión-Grant G, Yilmaz B, Grady C, Tanrikulu B, Bakircioğlu M, Kaymakçalan H, Caglayan AO, Sencar L, Ceyhun E, Atik AF, Bayri Y, Bai H, Kolb LE, Hebert RM, Omay SB, Mishra-Gorur K, Choi M, Overton JD, Holland EC, Mane S, State MW, Bilgüvar K, Baehring JM, Gutin PH, Piepmeier JM, Vortmeyer A, Brennan CW, Pamir MN, Kiliç T, Lifton RP, **Noonan JP**, Yasuno K, Günel M. Genomic analysis of non-NF2 meningiomas reveals mutations in TRAF7, KLF4, AKT1, and SMO. *Science* 339(6123):1077-80 (2013).

17: Oh S, Song S, Grabowski G, Zhao H, **Noonan JP**. Time series expression analyses using RNA-seq: a statistical approach. *Biomed. Res. Int.* 2013:203681 (2013).

18: DeMare LE, Leng J, Cotney J, Reilly SK, Yin J, Sarro R, **Noonan JP**. The genomic landscape of cohesin-associated chromatin interactions. *Genome Res.* 23(8):1224-34 (2013).

19: Cotney J, Leng J, Yin J, Reilly SK, DeMare LE, Emera D, Ayoub AE, Rakic P, **Noonan JP**. The evolution of lineage-specific regulatory activities in the human embryonic limb. *Cell* 154(1):185-96 (2013).

20: Pavlicev M, Wagner GP, **Noonan JP**, Hallgrímsson B, Cheverud JM. Genomic correlates of relationship QTL involved in fore- versus hind limb divergence in mice. *Genome Biol. Evol.* 5(10):1926-36 (2013).

21: Willsey AJ, Sanders SJ, Li M, Dong S, Tebbenkamp AT, Muhle RA, Reilly SK, Lin L, Fertuzinhos S, Miller JA, Murtha MT, Bichsel C, Niu W, Cotney J, Ercan-Sencicek AG, Gockley J, Gupta AR, Han W, He X, Hoffman EJ, Klei L, Lei J, Liu W, Liu L, Lu C, Xu X, Zhu Y, Mane SM, Lein ES, Wei L, **Noonan JP**, Roeder K, Devlin B, Sestan N, State MW. Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. *Cell* 155(5):997-1007 (2013).

22: Liu L, Lei J, Sanders SJ, Willsey AJ, Kou Y, Cicek AE, Klei L, Lu C, He X, Li M, Muhle RA, Ma'ayan A, **Noonan JP**, Sestan N, McFadden KA, State MW, Buxbaum JD, Devlin B, Roeder K. DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. *Mol. Autism* 5(1):22 (2014).

23: Cotney J, **Noonan JP**. Chromatin immunoprecipitation with fixed animal tissues and preparation for high-throughput sequencing. *Cold Spring Harb. Protoc.* 2015(4):419 (2015).

24: Cotney J, Muhle RA, Sanders SJ, Liu L, Willsey AJ, Niu W, Liu W, Klei L, Lei J, Yin J, Reilly SK, Tebbenkamp AT, Bichsel C, Pletikos M, Sestan N, Roeder K, State MW, Devlin B, **Noonan JP**. The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. *Nat. Commun.* 6:6404 (2015).

25: Reilly SK, Yin J, Ayoub AE, Emera D, Leng J, Cotney J, Sarro R, Rakic P, **Noonan JP**. Evolutionary changes in promoter and enhancer activity during human corticogenesis. *Science* 347 (6226):1155-9 (2015).

26: Emera D, Yin J, Reilly SK, Gockley J, **Noonan JP**. Origin and evolution of developmental enhancers in the mammalian neocortex. *Proc. Natl. Acad. Sci. USA* 113(19):E2617-26 (2016).

27: Sarro R, Emera D, Uebbing S, Dutrow EV, Weatherbee SD, Nottoli T, **Noonan JP**. Disrupting *Pitx1* regulatory topology results in overtly normal limb development. *bioRxiv* doi.org/10.1101/138644 (2017).

28: Wilderman A, Kron J, VanOudenhove J, **Noonan JP**, Cotney J. High resolution epigenomic atlas of early human craniofacial development. *bioRxiv* doi.org/10.1101/135368 (2017).

Invited Reviews

1: **Noonan JP**. Regulatory DNAs and the evolution of human development. *Curr. Opin. Genet. Dev.* 19(6): 557-64 (2009).

2: **Noonan JP**, McCallion AS. Genomics of long-range regulatory elements. *Annu. Rev. Genomics Hum. Genet.* 11:1-23 (2010).

3: Sholtis SJ, **Noonan JP**. Gene regulation and the origins of human biological uniqueness. *Trends Genet.* 26(3):110-8 (2010).

4: **Noonan JP**. Neanderthal genomics and the evolution of modern humans. *Genome Res.* 20(5):547-53 (2010).

5: Reilly SK, **Noonan JP**. Evolution of gene regulation in humans. *Annu. Rev. Genomics Hum. Genet.* 17:45-67 (2016).